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Perfect score:
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S52686 HLA class I
CQ806661 Sequence
AL929592 Human DNA
AC020768 Homo sapi
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ALIGNMENTS

### REFERENCE AUTHORS TITLE SOURCE ORGANISM DEFINITION ACCESSION VERSION KEYWORDS RESULT 1 BD273753 ORIGIN COMMENT FEATURES FOCUS Query Match Best Local Similarity Matches JOURNAL source GLAXO GROUP LTD OS Homo sapiens (human) PN JP 2002537843-A/1 PD 12-NOV-2002 PF 09-MAR-2000 JP 2000603406 PR 11-MAR-1999 GB 9905498.3 PI HERVE JEAN-CLEMENT COSTE, JONATHAN HENRY ELLIS PC C12N15/09, A61K38/44, A61K39/00, A61K48/00, C07K14/46, C12N5/10, PC C12P1/02, PC C12N15/00, C12N5/00, A61K37/50 CC Expression Location/Qualifiers FT source 1. 215 FT source (organism='Homo sapiens (human)'. 215; Expression Patent: JP Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 215) Coste, H.J. and Ellis, J.H. Homo sapiens BD273753.1 GI:33083521 JP 2002537843-A/1. Expression. BD273753 Homo sapiens (human) BD273753 Conservative JP 2002537843-A 1 12-NOV-2002; /organism='Homo /organism="Homo sapiens" /mol\_type="genomic DNA" /db\_xref="taxon:9606" 100.0%; Score 215; DB 6; 100.0%; Pred. No. 1.3e-46; rative 0; Mismatches 0; 215 đq DNA Length 215; Indels linear PAT 17-JUL-2003 0; Gaps g

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L patent: JP 2002537843-A 2 12-NOV-2002;
GLAXO GROUP LTD
OS Homo sapiens (human)
PN JP 2002537843-A/2
PD 12-NOV-2002
PF 09-MAR-2000 JP 2000603406
PR 11-MAR-1999 GB 9905498.3
PI HERVE JEAN-CLEMENT COSTE, JONATHAN HENRY ELLIS PC
C12N15/09, A61K38/44, A61K39/00, A61K48/00, C07K14/46, C12N5/10, PC
C12P1/02,
PC C12N15/00, C12N5/00, A61K37/50
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1 (Dases 1 to 215)

Coste, H. J. and Ellis, J. H.
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JP 2002537843-A/2.
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                TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
                                                                                CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
                                                                                                             GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTT
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/mol_type="genomic RNA"
/db_xref="taxon:9606"
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Pred. No. 1.3e-46;
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Patent: WO 0053785-A 2 14-SEP-2000;
COSTE HERVE JEAN CLEMENT (FR) ; GLAXO GROUP LTD (GB)
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Sequence 2 from Patent WO0053785
AX036039
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Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                          Homo sapiens (human)
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Patent: WO 0053785-A 1 14-SEP-2000;
COSTE HERVE JEAN CLEMENT (FR) ; GLAXO GROUP
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Sequence 1 from Patent WO0053785
AX036038
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Location/Qualifiers
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ilarity 100.0%;
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                              Conservative
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/mol_type="unassigned RNA"
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/mol_type="unassigned DNA"
/db_xref="taxon:9606"
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I21401
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Kowalski,J., Gilbert,S. and Zamb,T.J

Bovine heat shock promoter and uses

Patent: US 5981224-A 2 09-NOV-1999,

Location/Qualifiers
          1 (bases 1 to 533)

Kowalaki, J., Gilbert, S. and Zamb, T.J.

Bovine heat shock promoter and uses t

Patent: US 552184-A 2 28-MAY-1996;

Location/Qualifiers
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/mol_type="unassigned
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Pred. No. 1.2e-46;
; Mismatches 0;
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Matches 215; Conserv
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1 (bases 1 to 533)
Kowalski, J., Gilbert, S. and Zamb, T.J.
Bovine heat shock promoter and uses thereof
Patent: US 5733745-A 2 31-MAR-1998;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence
195741
Human cDNA encoding HSP70.
E12384
E12384.1 GI:3251217
JP 1996322577-A/1.
                                                E12384
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/mol_type="unassigned
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/mol_type="unassigned
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Pred. No. 1.2e-46;
0; Mismatches 0;
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Pred. No. 1.2e-46;
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01-DEC-1998

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L Patent: JP 199632577-A 1 10-DEC-1996;
HOKEN KAGAKU KENKYUSHO:KK
OS Homo sapiens (human)
PN JP 199632577-A/1
PD 10-DEC-1996
PF 01-UN-1995 JP 1995158581
PI DEMURA HIROSHI, NOMURA KAORU, SHIMIZU SHOICHI, PI R
TABURIYU HANKINZU,
PI HISAKAWA YOSHIZO
PC C12N15/09,c12P21/02,c12Q1/68;
CC strandedness: Double;
CC strandedness: Double;
FH Key Linear;
FH Key Linear;
FH Key Joganisme Homo sapiens'
FT CDS /product-HSP70'
FT mutation /product-HSP70'
FT mutation /one1ifiers /product-Splicing caused by
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1 (Dases 1 to 2465)

Demura,H., Nomura,K., Shimizu,S., Raari,T.H. and Hisakawa,Y.

TRANSCRIPTIONAL ABNORMALITY OF INTEACELLULAR HSP70KRNA UNDER
SUSTAINED STRESS LOAD CONTAINING HUMAN ACUTENESS AND CHRONICITY AI

ITS APPLICATION (APPLICATION OF BOTH TRANSCRIPTIONAL EXPRESSION ON THE HUMAN INTRACELLULAR SHSP70MRNA AND TRANSCRIPTIONAL ABNORMALIT
                                                       Homo sapiens (human)
Homo sapiens
                                                                                                 CQ812310
Sequence 62 from Patent
CQ812310
CQ812310.1 GI:47601930
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Wittig,R.,
                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; E
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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sapiens
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ition join(1. .143,306,,2465)
/note='alternative splicing caused by stress'.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
Poustka, A.,
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Mollenhauer,J.
                                                                                                                                 2691 bp DNA
WO2004038020.
and
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Schadendorf,D
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TITLE
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Sequence 6 from Patent WO2004039412.
CQ818823 CQ818823.1 GI:48427426
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                                                                                                                                                                                                                                                                                                                                                                                                                                                           Doiron,B., Pownall,S., Cheung,A. and Hsu,E. Compositions for cancer treatment Patent: WO 2004039412-A 6 13-MAY-2004;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                      CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTTCCAGCCCCCAA
                                                                                                 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTT
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                                                                            GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT
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                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="unassigned DN
/db_xref="taxon:9606"
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Pred. No. 1.1e-46;
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    Mol. Cell. Biol. 7 (3 87172780
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                                                  (bases 94 to 293)
Morgan, W.D., Williams, G.T., Morimoto, R.I., Greene, J., Kingston, R.I
and Tjian, R.
Two transcriptional activators, CCAAT-box-binding transcription
Two transcriptional activators, TCAAT-box-binding transcription
factor and heat shock transcription factor, interact with a human
                                                                                                                                                  Hunt.C. and Morimoto,R.I.

Conserved features of eukaryotic hsp70 genes revealed by with the nucleotide sequence of human hsp70 proc. Natl. Acad. Sci. U.S.A. 82 (19), 6455-6459 (1985)
                                                                                                                                                                                                                                                       HSP70 gene; heat shock protein.
Homo sapiens (human)
Homo sapiens
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Malkovsky,M. and Wells,A.D.
Immune response enhancer
Patent: US 6331388-A 1 18-DEC-2001;
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Sequence 1 from
AR262810
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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/mol_type="genomic DNA"
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'hep 70)
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                                                                                            Greene, J., Kingston, R.E.
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  Biochem.
99194576
                                                                                                                   Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                  variant, partial cds.
AB018045
AB018045.1 GI:4691417
AB070-1; heat shock protein 72; HSP70-Hom; alternative splicing.
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[2] revises [1]. Sequence revised July 30, 1992.
Location/Qualifiers
                                                         Shimizu, S., Nomura, K., Ujihara, M. and Demura, H. An additional exon of stress-inducible heat sho
                                                                                                                                                                                                                                                                         Homo sapiens HSP70-1 gene
                                         (HSP70-1)
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TDTERLIGDAARNQVALNPQNTVFDAKRLIGRKFGBDFVQSDKHWPFQVINDGDKFK

VQVSYKGETKARPYPEEISSMULTKKREIAEAVLGYFVTNAUITVPAYENBSQRQATKD

AGVIAGLAVLRIINEFTAAAIAYGLDRTGKGERNULIFDLGGGFTFDVSIITIDDGIFE

VRATAGDTHLGGEDFDNRLVNHFVEEFKRKHKKDISQNKRAVRERTAACERAKRTLSS

STQASLEIDSLFEGIDFYTSITRAFFEELCSDLFRSTLEPVEKALRDAKLDKAQIHDL

VLVGGSTRIFKVQKLLQDFFNGADLNKSINPDEAVGYGAAVQAAILMGDKSENVQDLL

LLDVAFLSGIEFTAGGVWTALIKRNSTIPTKQTGIFTTYSDNQDGVLLQVYEGERAMT

KLDVAFLSGIERAFQDEAKYKAEDEVQRERVSAKNALESYAFNMKSAVEDEGLKKKISDAKK

KKVLDKCQEVLSWLDANTLAEKDEFEHKRKELEQVCNPIISGLYQGAGGFGFGGFGAQ
                      Biophys. Res. Commun.
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/product="heat shock protein"
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/db_xref="GI:386785"
/db_xref="GDB:G00-120-058"
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489. .2411
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/note="70 kDa"
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/map="6p21.3"
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|mol_type="genomic DNA"
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S52686
HLA class III por
region} [human,
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Nomura, K. and Shimizu, S.
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2323. .4360
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complement(1. .196)
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2323. .2679
488 bp DNA linear PRI 08-MAY-1
III polymorphic region: HSP70-1=heat shock protein 70
human, PGF, WT49, WT51, Genomic, 488 nt).
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/gene="HSP70-1"
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1 (bases 1 to 488)
Cascino, I., Sorrentino, R. and Tosi, R.
Strong genetic association between HLA-DR3 and a polymorphic variation in the regulatory region of the HSP70-1 gene Immunogenetics 37 (3), 177-182 (1993)
93131289
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Sequence 111 from Patent
CQ806661
CQ806661.1 GI:47112043
                                                                                                            proliferative disorders
Patent: WO 2004035803-A
Epigenomics AG (DE)
                                                                                                                                                                                                                          Foekens,J., Harbeck,N., Koenig,T., Maier,S., Martens,J., Model,F., Nimmrich,I., Rujan,T., Schmitt,A., Schmitt,M., Look,M.P. and
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/db_xref="taxon:9606"
                                           /organism="Homo sapiens"
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/note="heat shock protein
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Pred. No. 1.6e-46;
1; Mismatches (
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The present sequence is the 5' untranslated region (UTR) of human heat shock protein (Hep) 70A gene. This sequence has a high potential to for secondary structures. This sequence can be used to increase the translation efficiency of a polypeptide. The present sequence may be useful in therapeutic or prophylactic vaccination for preventing

Human heat shock protein 5' untranslated region (UTR) transcribed to provide an RNA molecule having UTR that increases translation efficiency of polypeptides, useful for treating deficiency in expression of the polypeptide.

WPI; 2000-594331/56.

Claim 7; Page 28; 44pp; English.

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  The present sequence is the 5' untranslated region (UTR) mRNA of human heat shock protein (Hsp) 70A gene. This sequence has a high potential t form secondary structures. This sequence can be used to increase the translation efficiency of a polypeptide. The present sequence may be useful in therapeutic or prophylactic vaccination for preventing bacterial, viral and parasitic infections and also for treating immunerelated diseases and for contraceptive purposes. In addition the present
                                                                                                                                      Human heat shock protein 5' untranslated region (UTR) transcribed to provide an RNA molecule having UTR that increases translation efficiency of polypeptides, useful for treating deficiency in expression of the
                                                                                                                              of polypeptides, polypeptide.
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related diseases and for contraceptive purposes. In addition, the prese
sequence may be useful in gene therapy of various disorders such as
cancer, cardiovascular disorders and cystic fibrosis
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efficiency; vaccine; bacterial;
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                                                                                                                                                                                                                                                         215 BP;
 UCUCAGAGCCGAGCAGAGAGCAGGGAACCGC
                          TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCGC 215
                                                                           CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTTCCAGCCCCCAA
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                                                                                        antiparasitic;
                                                                                                  Human; hsp72;
                                                                                                                         Human hsp72 encoding sequence
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                                                                 Homo sapiens
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(WISC ) WISCONSIN ALUMNI RES

FOUND

17-OCT-1997;

97US-00955565

2002-138381/18

Increasing expression of an MHC class I molecule in a cell, useful in increasing antigen presentation and enhancing immune recognition of coinfected with pathogens, by expressing a heat shock protein introduced infected with pathogens, by expressing a heat shock protein introduced infected with pathogens, by expressing a heat shock protein introduced in the pathogens. introduced cells

Example 1; Fig 1; 89pp; English

This invention relates to increasing expression of an MHC class I molecule in a target cell, infected with a pathogen that is processed the MHC class I endogenous pathway. The method of expressing a HSP is achieved by the introduction of an expression vector encoding HSP to produce a transfected cell with increased expression of at least one M class I molecule. The method can be used to increase expression of an MHC class I molecule in a target cell and to increase expression of an antigen on a cell surface by an MHC class I molecule. The method can enhance the immunogenicity of the endogenous antigen in vivo, by enhancing the generation of antibodies to an otherwise poorly immunoge immunogenic an MHC one MHC á

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                adult respiratory distress syndrome; inflammatory bowel disease; Crohn's disease; ulcerative colitis; periodontal disease; granulocyte activation; chronic inflammation; allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      viral infection, parasitic infection, protozoal infection, fungal infection, sterile inflammatory disease, psorlasis, rheumatoid arthritis, glomerulonephritis, asthma, thrombosi cardiac reperfusion injury, renal reperfusion injury, ARDS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA differentially expressed in granulocytic cells #488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK83917;
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                                                                                   markers that
                                                                                                                                                                                                                                                 Beazer-Barclay
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                                                                                                    ting granulocyte activation by detecting differential expression associated with granulocyte activation, which serves as diagnost
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                                                                                                                                                                                                                                                                                                       GENE LOGIC INC
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                                                                                is useful
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Pred. No. 1.1e-54;
; Mismatches 0;
                                                                                                                                                                                                                                              Yamaga
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ftp.wipo.int/pub/published_pct_sequences
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Pred. No. 1.1e-54;
Mismatches 0;
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RESULT 5
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DT 01-J
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DE Huma
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EN Prec
XW gene
XX 01-JAN-2004 ADD14739 standard; cDNA; 2691 BP ADD14739; (first entry)

Human grc biomarker polynucleotide SEQ Ħ NO:133

predictor set; protein tyrosine kinase activity modulator; protein tyrosine kinase pathway; protein tyrosine kinase; cytostatic; gene therapy; drug sensitivity; genetic profile; cancer; human; gene; 88

Claim 1;

SEQ ID NO 488; 114pp; English

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CC polynuclectides or polypeptides whose expression pattern is predictive of the response of cells to treatment with a compound that modulates protein cyrosine kinase activity or members of the protein tyrosine kinase compounds. Also described: (1) predicting whether a compound is capable of pathway, Also described: (1) predicting whether a compound is capable of correlating the activity of cells, comprising obtaining a sample of cells, correlating the expression of the markers to the compound a sample of cells, correlate with compound sensitivity or resistance of cell lines for correlate with compound sensitivity or resistance of cells associated with a disease state; and (3) identifying polynuclectides and colypeptides whose expression pattern of cell lines to one or more compounds analysing the presistance of cells associated with a disease state, comprising subjecting the plurality of cell lines to one or more compounds, analysing the expression pattern of a microarray of polynuclectides or polypeptides, and selecting colypeptides have cytostated with a disease state by using the expression pattern of the microarray. The polynuclectides and colypeptides and polypeptides are useful in predicting the cativity of compounds that interact with protein tyrosine kinases and/or protein tyrosine kinase pathways. These may be used in determining drug cancer) based on patients to allow the development of individualized cancer) based on patient response at a molecular level. The present exquence is used in the exemplification of the present invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 215; DB 10; 100.0%; Pred. No. 1.1e-54; Live 0; Mismatches 0;
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181

TCTCAGAGCCGAGCGACAGAGAGCAGGGAACCG

214

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GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT

120 393

ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTTTTTTCGAGAGTGACTCCC

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                                                                                                         Matches
                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                  polypeptide compared to the level of the polypeptide in a subject free of cancer is indicative of cancer. The polypeptide is selected from any of the polypeptide is selected from any of the polypeptide is selected from any of specification and polypeptides which are at least 70% homologous to the polypeptides. The method of the invention has cytostatic activity, and may have a use in gene therapy. The method is useful in identifying markers specific for one or several types of cancer, depending on the tissue origin, which may be used in numerous diagnostic and prognostic applications as well as cancer type-specific targets for therapeutic intervention. The compounds that modulate the activity of a tumour suppressor gene are useful in the treatment of cancer or as anti-cancer suppressor gene are useful in the treatment of cancer or as anti-cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Diagnosing cancer comprises determining the polypeptide or polynucleotide levels e.g., hepatic lipase, in a sample from a subject, where a higher level compared to that in a subject free of cancer is indicative of
                                                                                                                                                                                                                                                           Sequence 2732 BP; 608 A; 787 C; 840 G; 497 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 subject, the method comprises determining, in a sample from the suithe level of at least one polypeptide, where a higher level of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 300; 272pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The invention relates to a novel method for diagnosing a cancer subject, the method comprises determining, in a sample from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (QUAR-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Feinstein E,
                                                                                                      214;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           QUARK BIOTECH INC
ATAACGGCTAGCCTGAGGAGCTGCTGCCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC
                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                     99.5%; Score 214; DB 10; 100.0%; Pred. No. 2.3e-54;
                                                                                                      <u>,</u>
                                                                                                         Mismatches
                                                                                                                                                                                Length 2732;
                                                                                                         Indels
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                                                                                                      Gaps
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RESULT 7
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                Chinding organic molecule that binds to the above polypeptide; (10) a CC composition of matter comprising the above (chimeric) polypeptide; (10) a CC composition of matter comprising the above (chimeric) polypeptide, CC antibody, oligopeptide or TAT binding organic molecule, in combination CC with a carrier; (11) an article of manufacture comprising a container and CC the composition of matter contained within the container; (12) methods of CC inhibiting the growth of a cell that expresses the above protein, where CC the growth of the cell is at least in part dependent upon a growth CC potentiating effect of the above protein; (13) a method of containing the growth of the cell is at sove protein; (13) a method of determining the protein CC cells that express the above protein; (14) a method of determining the protein CC disorder associated with increased expression or activity of the above CC protein; and (17) a method of binding an antibody, oligopeptide or companie mathod of containing and cell that expresses the protein described above.

CC The TAT sequences have cytostatic activities, and can be used in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide

sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region of

(a); (c) the complement of (a) or (b); (d) a sequence that has 80%

sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-

(c). Also described: (1) an expression vector comprising the above

nucleic acid; (2) a host cell comprising the above expression vector; (3)

a process for producing a polypeptide; (4) an isolated polypeptide

comprising: (a) an amino acid sequence encoded by any of the above

nucleotide sequences; (b) an amino acid sequence encoded by the full-

cuprising region of the above nucleotide sequences; or (c) a sequence

comprising the above polypeptide fused to a heterologous polypeptide;

comprising the above polypeptide fused to a heterologous polypeptide;

comprising the antibody that binds to the above polypeptide; (7) a process

comprising the antibody; (8) an isolated oligopeptide that binds to

the above polypeptide; (7) a process

comprising the antibody; (8) an isolated oligopeptide that binds to

the above polypeptide; (7) a process

comprising the antibody; (8) an isolated antigenic target (TAT)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tumour-associated antigenic target (TAT) cDNA sequence #4138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; SEQ ID NO 4138; 5504pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention describes an isolated tumour-associated antigenic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Wu TD,
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) WU T D.
) ZHOU Y.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Zhou Y;
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RESULT 8
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The present invention describes an isolated tumour-associated antigenic target (TAR) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding region (a); (c) the complement of (a) or (b); (d) a sequence that has 80% sequence identity to (a)-(c); or (e) a sequence that hybridises to (a)-(c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3 a process for producing a polypeptide; (4) an isolated polypeptide comprising: (a) an amino acid sequence encoded by any of the above
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      a medicament for the therapeutic treatment or diagnostic cell proliferative disorder or cancer. The present sequen human TAT cDNA sequence from the present invention.
                                                                                                                                                                               New nucleic acid molecule and encoded polypeptide, in preventing or treating cell proliferative disorders
                                                                                                                                                                                                                                                           Wu TD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     human; tumour-associated antigenic target; cancer; cell proliferative disorder; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human tumour-associated antigenic target (TAT) cDNA sequence #1793.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  preventing or treating cancer. The composition is also used for preparing
                                                                                                                                                  Claim 1; SEQ ID NO 1793; 5504pp; English.
                                                                                                                                                                                                                             WPI; 2004-534300/51
                                                                                                                                                                                                                                                                                       (GETH ) GENENTECH (WUTD/) WU T D. (ZHOU/) ZHOU Y.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cDNA sequence from the present invention.
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                                                                                                                                                                                                                                                                                                                     INC.
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Pred. No.
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ch as cancer
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RESULT 9
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clampth coding region of the above nucleotide sequences; or (c) a sequence
cc having at least 80% identical to (a) or (b); (5) a chimeric polypeptide
cc comprising the above polypeptide fused to a heterologous polypeptide; (6)
cc an isolated antibody that binds to the above polypeptide; (7) a process
cc for producing the antibody; (8) an isolated oligopeptide that binds to
cc composition of matter comprising the above polypeptide; (10) a
cc composition of matter comprising the above polypeptide; (10) a
cc composition of matter contained within the container; (11) an article of manufacture comprising a container and
cc the composition of matter contained within the container; (12) methods of
cc inhibiting the growth of a cell that expresses the above protein, where
cc the growth of the cell is at least in part dependent upon a growth
cc potentiating effect of the above protein; (13) a method of
cc therapeutically treating a mammal having a cancerous tumour comprising
cc cells that express the above protein; (14) a method of
cc greence of a protein in a sample suspected of containing the protein
cc described above; (15) methods of diagnosing the presence of a tumour in a
cc mammal; (16) a method for treating or preventing a cell proliferative
cc protein; and (17) a method of that expresses the above.
cc protein; and closure of a cell that expresses the protein described above.
cc protein; and cross have cytostatic activities, and can be used in gene
cc therapy. The composition and methods are useful for diagnosing,
cc preventing or treating cancer. The composition is also used for preparing
cc preventing or treating cancer. The composition is also used for preparing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity
Matches 214; Conserv
15-OCT-2003; 2003WO-US029126
                                                                                                                                                                                                                                                                                     human; tumour-associated antigenic target; TAT; cytostatic; gene therapy; cancer; cell proliferative disorder; gene; ss.
                                                                                                                                                                                                                                                                                                                                                                                                         Human tumour-associated antigenic target (TAT) cDNA sequence #616
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADQ83802 standard; cDNA; 2767
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 2767 BP; 621 A; 809 C; 853 G; 484 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       preventing or treating cancer. The composition is also used for preparing a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative disorder or cancer. The present sequence represents a
                                                                                                                                                  WO2004060270-A2
                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTTCCGTTTTCCAGCCCCCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TCTCAGAGCCGAGCGACAGAGAGCAGGGAACCG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCCGTTTCCAGCCCCCAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 214; DB 12;
Pred. No. 2.3e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length 2767;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Indels
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ATAACGGCTAGCCTGAGGAGCTGCTGCGACACTCCACTACCTTTTTCGAGAGTGACTCCC

GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGGTGCAGGCACCGGCGCGTCGAGTTT
CCGGCGTCCGGAAGGAACCGAGCTCTTCTCGCGGATCCAGTGTTCCGGTTTCCAGCCCCCAA

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cc (a); (c) the complement of (a) or (b); (d) a sequence that has 80% (c) the complement of (a) or (b); (d) a sequence that has 80% (e). CC (c). Also described: (1) an expression vector comprising the above nucleic acid; (2) a host cell comprising the above expression vector; (3) CC a process for producing a polypeptide; (4) an isolated polypeptide ccomprising; (a) an amino acid sequence encoded by the full-CC length coding region of the above nucleotide sequence encoded by the full-CC length coding region of the above nucleotide sequence encoded by the full-CC comprising the above polypeptide; (b) an amino acid sequence encoded by the full-CC comprising the above polypeptide fueld to a heterologous polypeptide; (c) composition of matter comprising the above polypeptide fueld to a heterologous polypeptide; (d) composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter comprising the above polypeptide; (10) a composition of matter contained within the container; (11) an article of manufacture comprising a container and composition to face cell is at least in part dependent upon a growth for the cell is at least in part dependent upon a growth cell fueld above protein; (13) a method of cells that express the above protein; (13) a method of determining the protein; and (17) a methods of diagnosing the presence of a tumour in a cell manufacture contained with increased expression or activity of the above protein; and contained that increased expression or activity of the above composition and method of binding an antibody, oligopeptide or composition and method are useful for diagnosing the protein of a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative diagnostic the above. The composition of a medicament for the therapeutic treatment or diagnostic detection of a cell proliferative diagnostic thereform the composition of a protein of a cell proliferative diagnostic detection of a cell prol
                                                                   Matches 214;
                                                                                       Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide sequences (see SEQ ID NO:1 to 4622); (b) the full-length coding (a); (c) the complement of (a) or (b); (d) a sequence that has a
                                                                                                                                                              Sequence 2767 BP; 621 A; 808 C; 854 G; 484 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention describes an isolated tumour-associated antigenic target (TAT) nucleic acid comprising: (a) any of 4622 nucleotide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 1; SEQ ID NO 616; 5504pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New nucleic acid molecule and encoded polypeptide, for diagnosing, preventing or treating cell proliferative disorders such as cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (GETH )
(WUTD/)
(ZHOU/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-OCT-2002; 2002US-0418988P.
                                                                                                                                                                                                             human TAT cDNA sequence from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENENTECH
WU T D.
ZHOU Y.
ATAACGGCTAGCCTGAGGAGCTGCTGCCGACAGTCCACTACCTTTTTCGAGAGAGTGACTCCC
                                                                 99.5%;
ilarity 100.0%;
Conservative (
                                                                   0
                                                                 Score 214; DB 13;
Pred. No. 2.3e-54;
0; Mismatches 0;
                                                                                                                                                                                                             the present invention.
                                                                   Indels
                                                                   <u>,</u>
                                                                   Gaps
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                                                                                                                                                                                                               The invention relates to a novel method for predicting the responsiveness of a subject with a cell proliferative disorder of the breast tissues to a therapy comprising analysing the methylation pattern of a target caid by contacting at least one of the target nucleic acids in a biological sample obtained from the subject prior to or during treatment. The method of the invention has cytostatic activity, and may have a use in gene therapy. The set of oligonucleotides comprising at least two of the oligomers are useful for detecting the cytosine methylation state and/or single nucleotide polymorphisms (SNPs) within the sequences. The methods, nucleic acid, oligonucleotide, and kit are useful for the creatment, characterisation, classification and/or differentiation, of breast cell proliferative disorders. The method is also useful for predicting the responsiveness of a subject with a cell proliferative CC disorder of the breast tissues to a therapy. The present sequence is used in the exemplification of the invention.
                                                                                                                        Matches
                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Foekens J, r
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Predicting responsiveness of a subject with breast cell proliferative disorder, useful for treating or differentiating breast cell proliferative disorders comprises analyzing methylation pattern of a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 111; 104pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          genomic DNA from the subject.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2004-348468/32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-OCT-2002; 2002DE-01045779
07-JAN-2003; 2003DE-01000096
17-APR-2003; 2003DE-01017955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-OCT-2003;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cytostatic; gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ds; gene; human;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human HSPA1A gene SEQ ID NO:111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADS89095 standard; DNA; 5387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (EPIG-) EPIGENOMICS AG
   2042
                                                              1982
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      181
                               61
 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT
                     GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCCGGCGCGCGTCGAGTTT
                                                           ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 2041
                                                                                     ATAACGGCTGAGGAGGAGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC
                                                                                                                                                                                          5387
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harbeck N,
Rujan T,
                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2003WO-EP010881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                                        BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cell proliferative disorder; breast; methylation; therapy; single nucleotide polymorphism; SNP.
                                                                                                                                                                                      1291 A; 1506 C;
                                                                                                                        99.5%; Score 214; DB 13;
100.0%; Pred. No. 2.7e-54;
tive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Koenig
Schmitt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ВP
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                                                                                                                                                                                      1471 G; 1119 T; 0 U; 0 Other,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maier S, M
Schmitt M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        575
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      214
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4, Look MP,
                                                                                                                                                     Length 5387;
                                                                                                                           Indels
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Marx A;
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                                           Query Match
Best Local Similarity
Matches 214; Conserv
                                                                                                                                                  The invention relates to a novel method for decreasing tumour mass in a cancer patient. The method comprises ablating bone marrow from the patient and grafting endothelial cell precursors (ECPs), or their precursors, into the patient such that a decrease in tumour mass results, where the ECPs or their precursors are genetically modified to mediate a decrease in tumour mass. The method of the invention has cytostatic activity. A polynucleotide of the invention acts as a tumour angiogenesis inhibitor, and may have a use in gene therapy and cell therapy. Genetically modified endothelial cell precursors are useful for decreasing tumour mass in a cancer patient. This is particularly useful for inhibiting and/or disrupting angiogenesis of the tumours, and consequently inhibiting tumour growth and killing tumour cells. The present sequence represents the 5' promoter region of the human hsp70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        gene; ds; human; tumour mass; cancer; bone marrow;
endothelial precursor; ECP; cytostatic;
tumour anglogenesis inhibitor; gene therapy; cell therapy; anglogenesis;
hsp70; promoter.
                                                                                                          Sequence
                                                                                                                                                                                                                                                                                                                                                                                Example 3; Fig 1; 34pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Decreasing tumor mass in a patient comprises grafting genetically modified endothelial cell precursors into the patient.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 2003-598707/56
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                West MD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human hsp70 gene 5'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-NOV-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADA45212 standard; DNA; 549 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-JAN-2002; 2002US-0349345P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JAN-2003; 2003WO-US001827
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO2003061591-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ADCE-) ADVANCED CELL TECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 121
ATAACGGCTAGCCTGAGGAGCTGCTGCGGACAGTCCACTTTTTTCGAGAGTGACTCCC
                                                                                                          549 BP; 110 A; 174 C; 167 G; 98 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTTCCGTTTTCCAGCCCCCAA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 2195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG
                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       promoter region
                                                          99.3%;
                                           0;
                                            Score 213.4;
Pred. No. 2.4e
0; Mismatches
                                                             213.4; DB 9;
No. 2.4e-54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  214
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AATS80HT 12
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ID AATS80
XX AATS8
XX Humar
XX Humar
XX Homo
XX AATS8
PT CDS
PT CCC CDS
CCC CDT
CC
                                                                                                                                                                                                                                                                                                        Query Match
Best Local S
Matches 214
                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         chronic sustained stress load
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present sequence, which encodes human heat shock protein 70 (HSP70), is located on human chromosome 6p 21.3-22 and 14q 22-24 and 21. Primers and probes based on the HSP70 cDNA coding sequence can be used to detect the abnormal transcription of intracellular HSP70 mRNA in human acute an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Fig 1; 13pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Detection of abnormal primer or probe, used stress load.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAW10065
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JUN-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-JUN-1995;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; heat shock protein 70; HSP70; primer; probe; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human heat shock protein 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 24-OCT-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HOKE-) HOKEN KAGAKU KENKYUSHO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          intracellular;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1997-081088/08.
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CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGGATCCAGTGTTCCGGTTTCCAGCCCCCAA
                                                                                 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT
                                                                                                                                    GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTCCAGGCACCGGCGCGTCGAGTTT
                                                                                                                                                                                                                                                ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                    BP; 553 A; 713
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
263. .2185
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Pred. No. 3.4
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Increasing glycogen to toxic levels in a cell, useful for treating ce proliferative disorder, comprises expressing in a cell a gene product that increases the amount of glycogen to toxic levels in the cell.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            increasing glycogen, toxic; toxic glycogen level; glycogen; cell proliferative disorder; tumour therapy; tumour; anti-tumour therapy; anti-cell proliferative; cytostatic; gene therapy; sarcoma; melanoma; myeloma; blastoma; glioma; lymphoma; leukaemia; human; heat shock protein 70; chromosome 6; hsp70; gene; ds.
                                                                                                                                                                                                                                                                       Example 1;
                                                                                                                                                                                                                                                                                                                               GENBANK;
                                                                                                                                                                                                                                                                                                                                         WPI; 2004-376072/35
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                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-2003; 2003WO-IB005562
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                                                                                                                                                                                                                                                                                                                                                                              (ENGE-)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TCTCAGAGCCGAGCCGACAGAGCAGCAGGGAACCGC 215
                                                                                                                                                                                                                                                                       SEQ ID NO 6; 98pp; English.
                                                                                                                                                                                                                                                                                                                                                           Pownall S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA;
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The present invention describes a method for increasing glycogen to toxic clevels in a cell. The method comprises expressing in a cell a gene comproduct that increases the amount of glycogen to toxic levels in the cell. Also described: (1) treating a cell proliferative disorder in a cell. Also described: (1) treating a cell proliferative disorder in a cell and the cell disorder, by expressing in one or more cells comprising the disorder in a cell glycogen, cell disorder, by expressing in one or more cells comprising the disorder with an agent that increases the amount of intracellular cell disorder with an agent that increases the amount of intracellular glycogen, sufficient to creat the cell proliferative disorder; (2) treating a subject that is conditionally or has undergone tumour therapy, where the tumour therapy was not for liver, muscle or brain tumour by administering to the subject an agent in an amount that increases the amount of intracellular glycogen in a cell; (3) increasing effectiveness of an anti-tumour therapy; (4) cell and the comprising the agent, and instructions for administering the agent to a subject in need or treatment on a label or packaging insert. (A) has cytostatic activity, and can be used in gene therapy. The methods are cell subject in need or treatment on a label or packaging insert. (A) has cytostatic activity, and can be used in gene therapy. The methods are custing a cell proliferative disorder, e.g. tumour, such as general sequence represents a translation enhancer element in the 5 cuntranslated region of a human heat shock protein 70 (hsp70) sequence comprising nucleotides 276 to 488 from the human hsp70 nucleotide from the present invention. Human hsp70 is located on chromosome 6, more specifically 6p21.3.

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RESULT 14
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Best Local S
Matches 213
              The invention relates to a novel method of identifying compounds that inhibit proliferation of cells comprising contacting a test compound with a cell which overexpresses Hsp72 (heat shock protein 72), and determining if the test compound inhibits activity or expression of Hsp72. Optionally, Hsp72 is contacted with the test compound under optimum conditions to allow the two components to interact and bind, forming a complex which is detected. The invention also relates to a method of identifying compounds that inhibit Hsp72-mediated JNK phosphatase activation, comprising contacting a test compound with a cell which expresses Hsp72, exposing the cell to a heat induced stress and determining if the compound inhibits JNK phosphatase activity. The
                                                                                                                                                                                                                                                                                                                                                                                                                  Identifying compounds that inhibit proliferation of cells and capable of modulating the expression of heat shock protein 72 gene and/or activity of Hap72 useful for treating cancers such as leukemia, lymphoma.
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Pred. No.
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                                                                                                                                                                                                                                                                                                                Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                         of Hsp72 or JNK phosphatase activity. The compounds identified as inhibitors of Hsp72 or JNK phosphatase activity are useful for inhibiting the proliferation of cells. Modulation of the activity of the JNK phosphatase or Hsp72 is used to treat a proliferative disorder such as cancers (e.g., laukaemia, lymphoma, solid tumours such as sarcomas and carcinomas, breast cancer, prostate cancer). The compounds that inhibit Hsp72 activity can also be administered to treat premalignant conditions and to prevent progression to a neoplastic or malignant state. The compounds that inhibit Hsp72 function are administered to a patient having a disease or disorder mediated by an increase of Hsp72 expression or activity relative to normal levels. The present sequence represents cDNA encoding human Hsp72 used in the exemplifications of the invention
                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2700
                                                                            394
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454
                                    181
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                                                                                                                                                                                                                                                                                                                213;
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                                                                                                    CCGGCGTCCGGAAGGACCCCAACCCCAA
                                                                                                                                                         GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT
                                                                                                                                                                               GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCTCGAGTTT
TCTCAGAGCGGAGCCGACAGAGCAGCAGGGAACCG
                                    TCTCAGAGCCGAGCCGACAGAGCAGCAGGGAACCG
                                                                            CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA
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                                                                                                                                                                                                                                                           ATAACGGCTAGCCTGAGGAGCTGCCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC
                                                                                                                                                                                                                                                                                                            98.8%; ilarity 99.5%; Conservative
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Pred. No. 6.9e-54;
                                                                                                                                                                                                                                                                                                                Mismatches
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487
                                    214
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RESULT 15
ADM02338
New polynucleotides and preveloping a diagnostic respression and activity,
                                                                                                               Seki N,
                                                                                                                                                                                                                                           12-APR-2002; 2002EP-00008400
                                                                                                                                                                                                                                                                                                          EP1347046-A1
                                                                                                                                                                                                                                                                                                                                                                                                       Human cDNA of the
                                                                                                                                                                                                                                                                                                                                                                                                                                         20-MAY-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADM02338;
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                                                                                                                                                                                                                                                                                                                                          Homo sapiens
                                                                  P-PSDB; ADM04781.
                                                                                                                                                                                                            22-MAR-2002; 2002JP-00137785
                                                                                                                                                                            (REAS-) RES ASSOC BIOTECHNOLOGY.
                                                                                                                              amamoto
                                                                                                                                                                                                                                                                                                                                                                        gene; human;
                                                                                 2003-723558/69.
                                                                                                               J, Isono
Yoshikawa
                                                                                                                                 Sugiyama T,
J, Isono Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                        gene
                                                                                                                                                                                                                                                                                                                                                                                                       invention SEQ ID NO:1023.
                                                                                                               Ήĸ
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                                                                                                                                                                                                                                                                                                                                                                      therapy;
                                                                                                             Otsuki T, Wakamatsu A, S
Hio Y, Otsuka K, Nagai K,
Otsuka M, Nagahari K, Mas
polypeptides are useful in gene therapy, marker or medicines for regulating their, or as a target of gene therapy.
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                                                                                                                                                                                                                                                                                                                                                                        diagnostic marker; pharmaceutical
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K, Irie
lasuho Y;
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Claim

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SEQ

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NO 1023;

for

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888888888888888 Ş 밁 Ş В Ş 밁 S Query Match Best Local Similarity Matches 211; Conserv The invention relates to a novel human polynucleotide and the encoded polypeptide. A polynucleotide of the invention may have a use in gene therapy. An oligonucleotide of the invention ADM06202-ADM06773 is useful as a primer for synthesizing the polynucleotide or as a probe for detecting the polynucleotide. The polynucleotides ADM01316-ADM03758 are useful in gene therapy, for developing a diagnostic marker or medicines for regulating their expression and activity, or as a target of gene therapy. The proteins ADM03759-ADM062701 encoded by the polynucleotides are useful as pharmaceutical agents. The present sequence represents a cDNA sequence of the invention. Sequence 1903 BP; 425 A; 531 C; 590 G; 181 183 121 123 61 63 H ω AACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGT TCAGAGCGGAGCCGACAGAGCAGCAGGAACCG 212 TCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214 GGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATC 180 GGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTTCCGGTTTCCAGCCCCCAATC TGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCCGTCGAGTTTCC 120 TGTCCCAAGGCTTCCCAGAGCGGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTTCC AACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGT Conservative 97.9%; 0 Score 210.4; DB 11; Length 1903; Pred. No. 2.6e-53; o; Mismatches 1; Indels 0; 357 T; 0 U; 0 Other; Gaps 60 62 182 122 0,

Search completed: February 11, 2005, 08:17:28 Job time : 224 secs

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Result
No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               OM nucleic - nucleic search, using sw model
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
      Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq length: 0
seq length: 2000000000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Issued Patents NA:*

1: /cgn2_6/ptodata/1.

2: /cgn2_6/ptodata/1.

3: /cgn2_6/ptodata/1.

4: /cgn2_6/ptodata/1.

5: /cgn2_6/ptodata/1.

6: /cgn2_6/ptodata/1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   IDENTITY NUC
Gapop 10.0 , Gapext 1.0
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215
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      1 ataacggctagcctgaggag.....gacagagagcagggaaccgc
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Copyright
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6A_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/backfiles1.seq:*
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US-07-975-719-2
US-08-599-825-2
US-08-048-488-2
US-09-918-039-144
US-09-919-039-145
US-09-919-039-145
US-09-976-799-719-1
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US-09-978-799-711869
US-09-913-294A-6467
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US-09-913-394A-6467
US-09-913-394-016-112336
US-09-949-016-125336
US-09-949-016-125336
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                    Sequence
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                    14, Appl
14, Appl
14, Appl
14, Appl
17, Appl
5, Appli
5, Appli
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17939, A
125345,
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1, Appli
11809, A
11869, A
11869, A
6467, Ap
4475, Ap
1221, Ap
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144, App
827, App
145, App
996, App
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2, Appli
1, Appli
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O	33	30.4	14.1	834	4	US-09-621-976-2574
ი	34	30.4	14.1	7719	4	US-09-902-540-969
ი	35	30	14.0	10419	4	US-09-408-020-3
ი	36	30	14.0	19157	4	US-09-949-016-13142
ი	37	30	14.0	42432	4	US-09-408-020-2
	38	29.6	13.8	601	4	US-09-949-016-30895
	39	29.6	13.8	601	4	US-09-949-016-30896
	40	29.6	13.8	601	4	US-09-949-016-105265
	41	29.6	13.8	601	4.	US-09-949-016-105266
	42	29.6	13.8	16572	4	US-09-949-016-12409
	43	29.6	13.8	16578	4	US-09-949-016-14680
	44	29.6	13.8	107800	4.	US-09-949-016-13118
	. <u>4</u> .		13.8	116425	4	110-00-010-016-11900

## ALIGNMENTS

RESULT 1 US-07-975-719-2

Sequence 2, Application US/07975719
PACENT NO. 5521084
GENERAL INFORMATION:
APPLICANT: KOWALSKI, JACEK
APPLICANT: GILBERT, SCOTT
APPLICANT: GILBERT, SCOTT
APPLICANT: BOYINE HEAT SHOCK PROMOTER AND USES
TITLE OF INVENTION: THEREOF

CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L NUMBER OF SEQUENCES:

```
CORRESPONDENCE ADDRESS:
ADDRESSE: ROBERTA L. ROBINS
STREET: 635 BRYANT STREET
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: UNITED STATES OF AMERICA
ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/975,719
FILING DATE: 19921113
CLASSIFICATION UMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 301-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
I-ENGTH: 533 base pairs
                                     Ś
                                                                                                                                                                         LENGTH: 533 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-07-975-719-2
밁
                                                                                  Query Match
Best Local Similarity
Matches 215; Conserv
                       ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTTCGAGAGTGACTCCC
ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTTCGAGAGTGACTCCC 294
                                                                                  100.0%; Score 215; DB 1; ilarity 100.0%; Pred. No. 5.6e-57; Conservative 0; Mismatches 0;
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/599,825
FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0003.01
TELECOMMUNICATION INFORMATION:
TELECOMOUNICATION INFORMATION:
TELEPHONE: (415) 327-3400
TELEPAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
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US-08-599-825-2
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Patent No. 5733745
                                                                                                                                                                                                         Matches 215;
                                                                                                                                                                                                                                       Query Match
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APPLICANT: KOWALSKI, JACEK
APPLICANT: GILBERT, SCOTT
APPLICANT: ZAMB, TIMOTHY J.
TITLE OF INVENTION: BOVINE HEAT SHOCK PROMOTER AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
LENGTH: 533 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
ADDRESSEE: ROBERTA L. ROBINS
STREET: 285 HAMILTON AVENUE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES:
                                                                                                                                                                                                                         Local Similarity
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STATE: CALIFORNIA
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                                                                                      GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT
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                                CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA 180
                                                                GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTT
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                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                           DNA (genomic)
                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                       Score 215; DB 1;
Pred. No. 5.6e-57;
Mismatches 0;
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Patent No.
                                                                                                                                                                                                                                                                       Matches
                                                                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/975,719
APPLICATION NUMBER: US/07/975,719
APPLICATION INFORMATION:
NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 53 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TITLE OF INVENTION: BOVINE HEAT SHOCK PROMOTER AND USES TITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,488
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ZIP: 94301
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                         MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                         LENGTH: 533 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
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                                                                                                 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTTCCGTTTTCCAGCCCCCAA 180
                                                                                                                                   GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT
                                                                                                                                                                     GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT
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TCTCAGAGCCGAGCGGACAGGGGAGCCGC 449
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                     TCTCAGAGCCGAGCCGACAGAGAGAGCAGGGAACCGC 215
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Pred. No. 5.6e-57;
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US-09-919-039-144
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; LENGTH: 2691
; TYPE: DNA
; ORGANISM: Homo sapiens
US-08-955-565A-1
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                                                                                                                                                                                                       ; NAME/KEY: misc_feature
; OTHER INFORMATION: Incyte ID No.
US-09-919-039-144
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                                                                                                                                                                                                                                                                                                            SEQ ID NO 144
LENGTH: 2412
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                                                                                                                                                     Query Match
Best Local Similarity
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CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Malkovsky, Miroslav
APPLICANT: Wells, Andrew
TITLE OF INVENTION: Immune Response Enhancer Therapy
FILE REFERENCE: WARF-02625
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/08/955,565A
CURRENT FILING DATE: 1997-10-17
NUMBER OF SEQ ID NOS: 6
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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mes 215; Conserv
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Pred. No. 1.7e-49;
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Pred. No. 8.7e-57;
                                                                                                                                     Mismatches
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CURRENT APPLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER OF SEQ ID NOS: 401
SOPTWARE: PERL Program
SEQ ID NO 145
LENGTH: 2458
TYPE: DNA
ORGANISM: Homo sapiens
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; LOCATION: 218..418
US-09-621-976-827
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Best Local S
Matches 210
                                                                                                                                                                                                   Sequence 145, Application US/09919039
PATENT NO. 6727066
GENERAL INFORMATION:
APPLICANT: Kaser, Matthew R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN
FILE REFERENCE: PA-0035 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PATENT NO. 6639063
GENERAL INFORMATION:
APPLICANT: Dumas Milne Edwards, J.B.
APPLICANT: Jobert, S.
APPLICANT: Glordano, J.Y.
TITLE OF INVENTION: ESTs and Encoded Human Proteins.
FILB REFERENCE: GENSET. 054PR2
CURRENT APPLICATION NUMBER: US/09/621,976
CURRENT FILING DATE: 2000-07-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 19335
SOFTWARE: Patent.pm
SEQ ID NO 827
LENGTH: 420
TYPE: DNA
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FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                     ATCTCAGAGCCGAGCGGACAGAGAGCAGGGAACCG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTYCCGTTTCCAGCCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTT 121
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CGAGCCGACAGAGAGCAGGGAACCG 214
                                                                                                                                                                                                                                                                                                                                                                                                  ATCTCAGAGCGGA-SCGACATAGAGCAGGGAACCG
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97.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 187.4; DB 4; Length 420;
Pred. No. 1.8e-48;
1; Mismatches 2; Indels 2
                                                                                                                                                                                                                                                                                                                                                                                                  215
                                                                                                                                                                                                                          C3A LIVER
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RESULT 9
US-07-975-719-1
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; NAME/KEY: misc_feature

; OTHER INFORMATION: Incyte ID No. 6673549 242010.60

US-09-976-594-996
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US-09-976-594-996
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; OTHER INFORMATION: Incyte ID No.
US-09-919-039-145
                                                                                                          Sequence 1, Application US/07975719
Patent No. 5521084
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/976,594
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: 60/240,409
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 1143
SOPTWARE: PERL Program
SEQ ID NO 996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 996, Applica Patent No. 6673549
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match 72.9%;
Best Local Similarity 88.5%;
Matches 170; Conservative
                                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Furness, Michael
APPLICANT: Buchbinder, Jenny
TITLE OF INVENTION: GENES EXPRESSED IN C3A LIVER CELL CULTURES TREATED WITH STEROIDS
FILE REFERENCE: PA-0041 US
APPLICANT: KOWALSKI, JACEK APPLICANT: GILBERT, SCOTT APPLICANT: ZAMB, TIMOTHY J.
TITLE OF INVENTION: BOVINE HITITLE OF INVENTION: THEREOF NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ENGTH: 1941
                                                                                                                                                                                                                                                                              143
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                                                                                                                                                                                                                                                                                                                 CGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCCGAAGGACTGAGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GCCTGAGGAGCTGCTGCGAGGGTCCGCTTCGTCTTTCGAGAGTGACTCCCGCGGTCCCAA 60
                                                                                                                                                                                                                                            TCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCCGAGCCCACAGAG
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                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                       46.1%;
89.2%;
 BOVINE HEAT SHOCK PROMOTER AND USES THEREOF 2
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Pred. No. 8.6e-39;
0; Mismatches 22
                                                                                                                                                                                                                                                                                                                                                                                       Score 99.2; DB 4;
Pred. No. 5.3e-21;
D; Mismatches 13
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RESULT 10
US-08-599-825-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 1, Application US/08599825 Patent No. 5733745
                                                ZIP: 94301

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/599,825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match 17.0%;
Best Local Similarity 66.0%;
Matches 68; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REGISTRATION NUMBER: 33,208
REFERENCE/DOCKET NUMBER: 9001-0003
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: ROBINS, ROBERTA L.
                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: ZAMB, TIMOTHY J.
TITLE OF INVENTION: BOVINE HEAT SHOCK PROMOTER AND USES
TITLE OF INVENTION: THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: KOWALSKI, JACE APPLICANT: GILBERT, SCOTT APPLICANT: ZAMB, TIMOTHY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/07/975,719
FILING DATE: 19921113
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MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
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CLASSIFICATION:
ATTORNEY/AGENT INI
                                                                                                                                                                                                                        STATE: C
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TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                             ADDRESSEE: ROBERTA L. ROBINS STREET: 285 HAMILTON AVENUE, CITY: PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STREET: 635 BRYA
                                      FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    552 GGCACCAGAGCGTTCAGTTTTCGGGTTCCGAAAAGCCCGAGCTTCTCGTCGCAGATCCTC 611
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                                                                                                                                                                                                                  CALIFORNIA
ONITED STATES
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  INFORMATION:
                                                                                                                                                                                                                           OF AMERICA
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Pred. No. 0.096;
                                                                                                                                                                                                                                                                                      SUITE
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                                                                                                                                                                                                                                                                                      200
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ROBINS, ROBERTA

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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEPHONE: (415) 327-3400
TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO: 1:
                                                                                  TELEFAX: (415) 327-3231
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION:
                                                                                                                                    NAME: ROBINS, ROBERTA L.
REGISTRATION NUMBER: 31,208
REFERENCE/DOCKET NUMBER: 90
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 617-8999
                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/0
APPLICATION NUMBER: US/0
FILING DATE: 1992-11-13
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/048,488
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
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   MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 750 base pairs TYPE: nucleic acid STRANDEDNESS: single TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                    TOPOLOGY:
                                 STRANDEDNESS:
                                                                                                                                                                                                                                                                                                    CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                        FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 33
REFERENCE/DOCKET NUMBER:
                                                                       LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       612
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                94301
                                               I: 750 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PALO ALTO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Application US/09048488
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KOWALSKI, JACEN
KOWALSKI, JACEN
KOWALSKI, JACEN
GILBERT, SCOTT
GAMB, TIMOTHY J.
TAMBH, TIMOTHY J.
SAWB, TIMOTHY J.
SAWB, TIMOTHY J.
TAMBH BOYING HEAT SHOCK PROMOTER AND USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: ROBERTA L. ROB
635 BRYANT STREET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                UNITED STATES OF AMERICA
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                      linear
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DNA (genomic)
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Query Match
Best Local Similarity
Matches 68; Conserv
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US-09-252-991A-11869/c
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                                                                                                                  NUMBER OF SEQ ID NOS:
SEQ ID NO 11869
LENGTH: 1320
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SEQ ID NO 11809
Query Match
Best Local Similarity
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                                                                                                                                                                                                                FILE REFERENCE: 107196.136
CURRENT APPLICATION NUMBER: US/09/252,991A
CURRENT FILING DATE: 1999-02-18
PRIOR APPLICATION NUMBER: US 60/074,788
PRIOR FILING DATE: 1998-02-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Marc J.
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                          PRIOR FILING DATE: 1998-02-18
PRIOR APPLICATION NUMBER: US 60/094,190
PRIOR FILING DATE: 1998-07-27
                                                                                                                                                                                                                                                                                                             APPLICANT: Marc J. Rubenfield et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: AERUGINOSA FOR DIAGNOSTICS A
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                                                                                              TYPE: DNA
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                                                                             ORGANISM: Pseudomonas aeruginosa
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les 57; Conserv
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NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING AERUGINOSA FOR DIAGNOSTICS AND THERAPEUTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            UMBER: US 60/074,788
1998-02-18
UMBER: US 60/094,190
1998-07-27
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15.6%;

Score 33.6; DB 4; Pred. No. 0.95;

Length 1320;

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Sequence 6467, Application US/09313294A

Patent No. 6476212

GENERAL INFORMATION:
APPLICANT: Lalgudi, Raghunath V.
APPLICANT: Ito, Laura Y.
APPLICANT: Sherman, BATANICLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR TITLE OF INVENTION: POLYNICLEOTIDES AND POLYPEPTIDES DERIVED FROM CORN EAR FILE REFERENCE: PL-0017 US
CURRENT APPLICATION NUMBER: US/09/313,294A

CURRENT FILING DATE: 1999-05-14

NUMBER OF SEQ ID NOS: 7600
SOFTWARE: PERL Program
SEQ ID NO 6467
LENGTH: 205
TYPE: DNA
ORGANISM: Zea may8
                                    LENGTH: 1728
; TYPE: DNA
; ORGANISM: Myxococcus
US-09-902-540-4475
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US-09-902-540-4475/c
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; LOCATION: 31, 178, 202-203
; OTHER INFORMATION: a, t, c,
US-09-313-294A-6467
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US-09-313-294A-6467
                                                                                                      GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CCURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10
NUMBER OF SEQ ID NOS: 16825
SEQ ID NO 4475
                                                                                                                                                                                                                                                                                                                                                    Sequence 4475, Application US/09902540 Patent No. 6833447
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NAME/KEY: misc feature
OTHER INFORMATION: Incyte ID No. 6476212 700351854H1
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Local Similarity 68.2%;
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 Score 32.4;
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Length 1728;
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                                                                        1568 GCCTGCCGCGCGGTCCGCCAGCGCCGTCTCACCCATGGAGCCGTGGATGCGCGTCAGG
                            136 ACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCC 177
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                                                                                                        76 CCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCGGAAGG 135
GCCAGGTGGATTTCCGGGTCGAACGGGTCCGACGCCAGCGCC 1467
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0; Mismatches
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Search completed: February 11, 2005, 09:04:16 Job time : 89 secs

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Minimum
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Maximum Match 100%
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                      and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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215
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1: /cgn2_6/ptodatta/1/pubpna/US07_PUBCOMB.seq:*

2: /cgn2_6/ptodatta/1/pubpna/PCT_NEW_PUB.seq:*

3: /cgn2_6/ptodatta/1/pubpna/US06_PUBCOMB.seq:*

4: /cgn2_6/ptodatta/1/pubpna/US06_PUBCOMB.seq:*
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: /cgn2_6/ptcdata/1/pubpna/PCTUS_PUBCOMB.seq:*
: /cgn2_6/ptcdata/1/pubpna/USO8_PUBCOMB.seq:*
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: /cgn2_6/ptcdata/1/pubpna/USO8_PUBCOMB.seq:*
: /cgn2_6/ptcdata/1/pubpna/USO9B_PUBCOMB.seq:*
: /cgn2_6/ptcdata/1/pubpna/USO9B_PUBCOMB.seq:*
: /cgn2_6/ptcdata/1/pubpna/USO9S_PUBCOMB.seq:*
: /cgn2_6/ptcdata/1/pubpna/USO9S_PUBCOMB.seq:*
: /cgn2_6/ptcdata/1/pubpna/USO9S_PUBCOMB.seq:*
: /cgn2_6/ptcdata/1/pubpna/USOSS_PUBCOMB.seq:*
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SUMMARIES  Query Query Query Match Length DB ID  99.5 2732 18 US-10-335-053-291 99.3 549 17 US-10-348-359-1 97.9 1903 17 US-10-108-260A-1023 90.7 2387 17 US-10-172-118-1144 90.7 2387 17 US-10-342-887-1144 90.7 2387 17 US-10-342-887-1144 90.7 2387 18 US-10-342-887-1144 76.1 506 16 US-10-919-039-144 76.1 506 16 US-10-029-386-6557 73.6 284 18 US-10-425-115-8988

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9807 9930 10122 62805	2636 2940917 2940917 1473 2261 7789 9698	583 584 584 939		595 595 596 596 9899 3673778 3673778 595 595	2771
17 17 17	13 13 17 17 17 17 17	18 18 18 18	15 16 18 18 18	18 118 118 118 118 118	17
US-10-379-381-1 US-10-210-130-33 US-10-210-130-35 US-10-379-381-3	US-10-002-600-95 US-10-027-632-174763 US-10-027-632-174763 US-10-027-632-174763 US-10-282-122A-14406 US-10-389-566-273 US-10-333-314-38 US-10-333-314-38 US-10-210-130-37	US-10-363-345A-17428 US-10-363-345A-20735 US-10-363-345A-20736 US-10-363-345A-20733 US-10-363-345A-20733 US-10-363-345A-20734 US-10-269-386-20724	US-10-311-455-2416 US-10-312-841-1 US-10-370-7158-21 US-10-363-345A-17425 US-10-363-345A-17426 US-10-363-345A-17427	-10-363- -10-363- -10-363- -10-363- -10-3112 S-10-3112 S-10-363- -10-363- -10-363-	US-10-027-632-111980
35°2°	<b></b>	Sequence 17428, A Sequence 20735, A Sequence 20736, A Sequence 20734, A Sequence 20734, A Sequence 20724, A	2416, A e 1, App 21, App 17425, 17426, 17427,		Sequence 111980,

# ALIGNMENTS

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SEQ ID NO 291
LENGTH: 2732
TYPE: DNA
ROANISM: Homo sapiens
US-10-335-053-291
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US-10-335-053-291
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Publication No. US20040241653A1
GENERAL INFORMATION:
APPLICANT: Quark Biotech, Inc.
TITLE OF INVENTION: Methods for identifying marker genes for cancer
FILE REFERENCE: 68733-A; 070/US1
                                                                                                                                                                                                              Matches
                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION NUMBER: US/10/335,053
CURRENT FILING DATE: 2003-03-27
PRIOR APPLICATION NUMBER: 60/345,317
PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 319
                                                                                                                                                                                                              214;
                     121
                                                                                                                                     274
                                                                                               61
CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTTCCAGTCTTCCAGCCCCCAA 180
                                                                                       GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCCGGCGCGCTCGAGTTT 120
                                                                                                                                                         ATAACGGCTAGCCTGAGGAGCTGCTGCGGACAGTCCACTTTTTTCGAGAGTGACTCCC
                                                         GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCGTCGAGTTT
                                                                                                                                     ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 333
                                                                                                                                                                                                        99.5%; (milarity 100.0%; Conservative 0;
                                                                                                                                                                                                            Score 214; DB 18; ; Pred. No. 2.4e-60; 0; Mismatches 0;
                                                                                                                                                                                                                                                  Length 2732;
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                                                             393
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60

180

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Sequence 1023, Application US/10108260A

PUBLICATION NO. US20040005560A1

GENERAL INFORMATION:
APPLICANT: HELIX RESEARCH INSTITUTE
TITLE OF INVENTION: NO. US20040005560A1el full length cDN
FILE REFERENCE: H1-A0106
CURRENT APPLICATION NUMBER: US/10/108,260A
CURRENT FILING DATE: 2002-03-27
NUMBER OF SEQ ID NOS: 5458
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1023
LENGTH: 1903
TYPE: DNA
CORGANISM: Homo sapiens
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US-10-108-260A-1023
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: WEST, MICHAEL

TITLE OF INVENTION: STEM CELL-DERIVED ENDOTHELIAL CELLS MODIFIED TO DISRUPT

TITLE OF INVENTION: TUMOR ANGIOGENESIS

FILE REFERENCE: 100375.54374US

CURRENT PELLICATION NUMBER: US/10/348,359

CURRENT FILING DATE: 2003-01-22

PRIOR APPLICATION NUMBER: 60/349,345

PRIOR FILING DATE: 2002-01-22

PRIOR FILING DATE: 2002-01-22

NUMBER OF SEQ ID NOS: 6

SOCTWARE: PATENTIN VET: 2.1

SEQ ID NO 1

LENGTH: 549

TYPE: DNA

ORGANISM: Homo sapiens

ORGANISM: Homo sapiens
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Publication No. US20040018178A1
GENERAL INFORMATION:
                                                          Query Match
Best Local Similarity
Matches 211; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
Matches 214; Conserv
                                                                                                                                                          -10-108-260A-1023
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                             3 AACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTTTTTTCGAGAGTGACTCCCGT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAA
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  Conservative
                                                                       Conservative
                                                                                         97.9%;
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99.5%; Pred. No. 3.46
tive 0; Mismatches
                                                                     0; Mismatches
                                                                                         Score 210.4; DB 1
Pred. No. 3.6e-59;
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.3.4e-60;
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                                                                                                           DB 17; Length 1903;
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APPLICANT: Dai, Hongyue
APPLICANT: He, Yudong
APPLICANT: Linsley, Peter
APPLICANT: He, Yudong
APPLICANT: Mao, Mao
APPLICANT: Mao, Mao
APPLICANT: Wan 't Veer, Laura
APPLICANT: Van 't Veer, Laura
APPLICANT: Van de Vijver, Marc
APPLICANT: Diagnosis and Prognosis of Breast Cancer Patients
TITLE OF INVENTION DIAgnosis with Prognosis of Breast Cancer Patients
TITLE OF INVENTION NUMBER: US/10/172,118
CURRENT FILING DATE: 2002-06-14
PRIOR APPLICATION NUMBER: 60/380,770
PRIOR APPLICATION SUMBER: 60/380,770
PRIOR APPLICATION SUMBER: 60/380,770
PRIOR FILING DATE: 2002-05-14
NUMBER OF SEG ID NOS: 2699
SEQ ID NO 1144
LENGTH: 2387
RESULT 5
US-10-342-887-1144
US-10-342-887-1144, Application US/10342887; Sequence 1144, Application US/10342887; Publication No. US20040058340A1; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue; APPLICANT: He, Yudong; APPLICANT: Linsley, Peter S.
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US-10-172-118-1144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 195;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
ORGANISM: Homo sapiens
PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DATABASE ACCESSION NUMBER: NM 005345
DATABASE ENTRY DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20 GCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAAGGCTTCCCA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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Gaps

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US-09-919-039-144
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; ORGANISM: Homo sapiens
US-10-342-887-1144
                                                                                                                                                   US-09-919-039-144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 195
                                                                                                                                                                                                                                                   GENERAL INFORMATION:
APPLICANT: KASEY, MAILTHEW R.
APPLICANT: KASEY, MAILTHEW R.
TITLE OF INVENTION: GENES EXPRESSED IN TREATED HUMAN C3A LIVER CELL CULTURES
FILE REFERENCE: PA-0035 US
CURRENT PELLICATION NUMBER: US/09/919,039
CURRENT FILING DATE: 2002-09-09
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR APPLICATION NUMBER: 60/222,113
PRIOR FILING DATE: 2000-07-28
NUMBER: OF SEQ ID NOS: 401
SOFTWARE: PERL PROGram
SEQ ID NO 144
LENGTH: 2412
TYPEE: NUMBER: PERL PROGram
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/380,710
PRIOR FILING DATE: 2002-05-14
PRIOR APPLICATION NUMBER: 10/172,118
PRIOR FILING DATE: 2002-06-14
NUMBER OF SEQ ID NOS: 2699
SEQ ID NO 1144
LENGTH: 2387
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 144, Appropriate Publication No.
                                                                     Matches
                                                                                                            Query Match
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APPLICANT:
APPLICANT:
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APPLICANT: Bernards, Rene
TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
FILE REFERENCE: 9301-188-999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: 60/298,918 PRIOR FILING DATE: 2001-06-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/342,887
CURRENT FILING DATE: 2003-01-15
                                                                                                                             FEATURE:
NAME/KRY: misc feature
NAME/KRY: misc feature
OTHER INFORMATION: Incyte ID No. US20030108871A1 242010.16
                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
mes 195; Conserv
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                                                                                          Similarity
                   GCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCCGTTGTCCCAA 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAGAGCAGGGAACCG 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GAGCGAACCTGTGCGGCTGCAGGCACCGGCGTCGAGTTTCCGGCGTCCGGAAGGACCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AGCTCTTCTCGCGGATCCAGTGTTCCGTTTCCAGCCCCCAATCTCAGAGCCGAGCCGACA
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GCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCCGTTGTCCCAA
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D. US20030108871A1
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                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Christopher J.
eer, Laura Johanna
                                                                                       89.0%;
                                                                         0
                                                                     Score 191.4; DB 1
Pred. No. 6.4e-53;
0; Mismatches 1
                                                                                                        DB 10;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: Annomax Sequence Listing Engine vers. SEQ ID NO 6557
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 6557, Application US/10029386 Publication No. US20030194704A1
                                                                                                                                                                                                                                                                                                                                                                                              Matches 178;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Rank, David R.
APPLICANT: Hanzel, David K.
APPLICANT: HANZEL DAVID K.
TITLE OF INVENTION: EXPRESSION ANALYSIS TWO
FILE REFERENCE: AEOMICA-X-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS: 34288
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CURRENT FILING DATE: 2001-12-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OTHER INFORMATION: MAP TO AF134726.1
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 5.5
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 4.8
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 3.1
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 11
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.9
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 7.9
OTHER INFORMATION: SWISSPROT HIT: POBLOT, EVALUE 2.00e-17
OTHER INFORMATION: NT HIT: M59830.1, EVALUE 0.00e+00
OTHER INFORMATION: EST_HUMAN HIT: BG773197.1, EVALUE 0.00e+00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
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                                                                                                                                                                                          CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGGATCCAGTGTTCCGGTTTCCAGCCCCCAA 180
                                                                                                                                                                                                                                                           GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGCTCGAGTTT
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                                                                                                                                                                                                                                       GCGGTCCCAAGGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTT
                                                                                                                                                                                                                                                                                                                  AAAACGGCCAGCCTGAGGAGCTGCTGCGAGGGTTCCGTTTTCGAGAGTGACTCCC 280
                                                                                                                                                                                                                                                                                                                                       ATAACGGCTAGCCTGAGGAGGCTGCTGCGACAGTCCACTACCTTTTTTCGAGAGAGTGACTCCC
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                                                                               TCTCAGAGCGGAGCCCACAGAG
                                                                                                                    TCTCAGAGCCGAGCCGACAGAG 202
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                                                                                                                                                                                                                                                                                                                                                                                              Conservative
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88.1%;
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                                                                                                                                                                                                                                                                                                                                                                                            Score 163.6; DB 1
Pred. No. 7.9e-44;
0; Mismatches 24
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Sequence 89981, Application US/10425115
Publication No. US20040214272A1
GENERAL INFORMATION:
APPLICANT: La ROSa, Thomas J.
APPLICANT: Kovalic, David K.

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GENERAL INFORMATION:

APPLICANT: KASEC, MATTHEW R.

FILT REFERENCE: PA-0035 US

CURRENT APPLICATION NUMBER: US/09/919,039

CURRENT FILING DATE: 2002-09-09

PRIOR APPLICATION NUMBER: 60/222,113

PRIOR FILING DATE: 2000-07-28

NUMBER OF SEQ ID NOS: 401

SOFTWARE: PERL Program

SOFTWARE: PERL Program

SEQ ID NO 145

SEQ ID NO 145

LENGTH: 2458
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, OTHER INFORMATION: Incyte
US-09-919-039-145
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TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT APPLICATION NUMBER: US/10/425,115
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 89981
LENGTH: 284
TYPE: DNA
ORGANISM: Zea mays
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 145, Application US/09919039 Publication No. US20030108871A1
                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                          TYPE: DNA ORGANISM: Homo sapiens FEATURE:
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                                                   GAAGGACCGAGCTCTTCTCGCGGGATCCAGTGTTCCGTTTTCCAGCCCCCAATCTCAGAGCC 190
                                                                                                                                                                                         GCCTGAGGAGCTGCTGCGACAGTCCCACTTTTTTCGAGAGTGACTCCCGTTGTCCCAA
   GAGCCGACAGAG 202
                                 GAAGGACTGAGCTCTTGTCGCGGATCCCGTCCGCCGTTTCCAGCCCCCAGTCTCAGAGCG
                                                                                                 GGCTTTCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGTGTTGAGTTTCCGGCGTTCC 120
                                                                                                                                  GGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTTCCGGCGTCCG
                                                                                                                                                                    GCCTGAGGAGCTGCGAGGGTCCGCTTCGTCTTTCGAGAGTGACTCCCGCGGTCCCAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CGTTTCCAGCCCCAATCTCATAGCGGAGCCGACAGATAGCAGGATCCGGC 171
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Cao, Yongwei
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                                                                                                                                                                                                                                                       72.9%;
88.5%;
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Pred. No. 4.5e-42;
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Pred. No. 1.5e-41;
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                                                                                                                                                                                                                                       Mismatches
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                                                                                                                                                                                                                                                                     DB 10;
                                                                                                                                                                                                                                       22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HUMAN C3A LIVER CELL
                                                                                                                                                                                                                                       Indels
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FILE REFERENCE: 108827.129

CURRENT APPLICATION NUMBER: US/10/027,632

CURRENT FILING DATE: 2002-04-30

PRIOR APPLICATION NUMBER: US 60/218,006

PRIOR PILING DATE: 2000-07-12

PRIOR APPLICATION NUMBER: US 60/198,676

PRIOR FILING DATE: 2000-04-20

PRIOR PILING DATE: 2000-04-20

PRIOR APPLICATION NUMBER: US 60/193,483

PRIOR FILING DATE: 2000-03-29

PRIOR PILING DATE: 2000-02-24

PRIOR PILING DATE: 1999-11-23

PRIOR PILING DATE: 1999-11-23

PRIOR APPLICATION NUMBER: US 60/167,363

PRIOR PILING DATE: 1999-02-28

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/156,358

PRIOR APPLICATION NUMBER: US 60/146,002

PRIOR PILING DATE: 1999-09-28

PRIOR PILING DATE: 1999-08-09

NUMBER OF SEQ ID NOS: 325720

SOPTWARE: FastSEQ for Windows Version 4.0
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US-10-027-632-111980/c
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; ORGANISM: Homo sapiens
US-10-335-053-290
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US-10-335-053-290
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Matches
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APPLICANT: Wang, David G.
TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: TO THE TOTAL OF T
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SEQ ID NO 290
LENGTH: 2513
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PRIOR FILING DATE: 2001-12-31
NUMBER OF SEQ ID NOS: 319
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TITLE OF INVENTION: Methods for
FILE REFERENCE: 68733-A; 070/US1
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CURRENT FILING DATE: 2003-03-27
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les 170; Conserv
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181 GAGCCCACAGAG 192
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Pred. No. 1.5e-41;
0; Mismatches 22;
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CURRENT FILING DATE: 2002-04-30
PRIOR APPLICATION NUMBER: US 60/218,006
PRIOR FILING DATE: 2000-07-12
PRIOR PPLICATION NUMBER: US 60/198,676
PRIOR FILING DATE: 2000-04-20
PRIOR FILING DATE: 2000-03-29
PRIOR PPLICATION NUMBER: US 60/193,483
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/185,218
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR APPLICATION NUMBER: US 60/167,363
PRIOR FILING DATE: 1999-01-23
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR FILING DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/166,358
PRIOR PILLNG DATE: 1999-09-28
PRIOR APPLICATION NUMBER: US 60/146,002
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; ORGANISM: Human
US-10-027-632-111980
                                                                                                                                                                                                                                                                                                              ; ORGANISM: Human US-10-027-632-111980
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SOFTWARE: FastSEQ for Windows Version
SEQ ID NO 111980
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Best Local Similarity
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Best Local Similarity
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TITLE OF INVENTION: Identification and Mapping of Single Nucleotide
TITLE OF INVENTION: Polymorphisms in the Human Genome
FILE REFERENCE: 108827.129
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR FILING DATE: 1999-08-09
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                        121 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCA 158
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99.4%;
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RESULT 13

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; OTHER INFORMATION: chemically treated genomic DNA; OTHER INFORMATION: CpG-island No: 17430 US-10-363-345A-17430
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Publication No. US20040234960A1
GENERAL INFORMATION:
APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/363,345A
CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
SEQ ID NO 17430
LENGTH: 595
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Publication No. US20040234960A1
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Best Local Similarity
Matches 171; Conserv
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LENGTH: 595
TYPE: DNA
                                                                          Matches
                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: Method for determining the degree of methylation of defined TITLE OF INVENTION: cytosines in genomic DNA in the sequence context of 5'-CpG-3 FILE REFERENCE; E01/1227
                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Alexander Olek
APPLICANT: Christian Piepenbrock
APPLICANT: Kurt Berlin
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CURRENT FILING DATE: 2003-03-03
NUMBER OF SEQ ID NOS: 40712
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: chemically treated genomic DNA
OTHER INFORMATION: CpG-island No: 17429
                                                                                                                                                                                                                      TYPE: DNA
ORGANISM: Artificial Sequence
                                                                                                                                                                                                           FEATURE:
                                                                      Local Similarity
les 171; Conserv
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ATRACGACTAACCTAAAAAACTACTACGACAATCCACTACCTTTTTCGAAAATAACTCCC
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D; Mismatches 43
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Search completed: February 11, 2005, 09:47:21 Job time : 265 secs
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Pred. No. 8.9e-38;
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BP231177	CB155190	CB133518	CB153107	BP382960	CB152693	CB152005	CB133993	CB138598	CB137829	CB138961	CB134000	CB133452	СВ133251	CB137170	BI548281	CB133685	CB133590	BM822968	AU076824	BP232134
BP231177	K-EST021	K-EST018	K-EST021	BP382960	K-EST020	K-EST020	K-EST018	K-EST019	K-EST019	K-EST019	K-EST018	K-EST018	K-EST018	K-EST0189	60319114	K-EST018	K-EST018	K-EST009	AU076824	BP232134

ALIGNMENTS

### RESULT 1 CN397686 LOCUS DEFINITION VERSION KEYWORDS REFERENCE 밁 Ş ORIGIN COMMENT SOURCE FEATURES ACCESSION Query Match Best Local S Matches 214 ORGANISM JOURNAL TITLE AUTHORS source 214; 78 230 Constitution Drive, Menlo Park, CA 94025, USA Tel: 650 473 8658 Fax: 650 473 7760 Email: rbrandenberger@geron.com Insert Length: 642 Std Error: 0.00. Location/Qualifiers Transcriptome characterization elucidates signaling networks control human ES cell growth and differentiation Nat. Biotechnol. 22 (6), 707-716 (2004) Contact: Brandenberger R Brandenberger,R., Wei,H., Zhang,S., Lei,S., Murage,J., Li,Y., Xu,C., Fang,R., Guegler,K., Rao,M.S., Mandalam, Lebkowski,J and Stanton,L.W. Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 642) 17000532601385 GRN\_ES Homo CN397686 Regenerative Medicine Geron Corporation Homo sapiens CN397686.1 GI:47385281 CN397686 Homo sapiens (human) Similarity ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTACCTTTTTCGAGAGTGACTCCC 99.5%; Suitarity 100.0%; ! Conservative 0; /clone\_lib="GRN\_ES" /note="oligo dT primed, full-length enriched cDNA library from undifferentiated hES cell lines H1 (p32), H7 (p29), and H9 (p26) maintained in feeder-free conditions" /organism="Homo sapiens" /mol\_type="mRNA" /db\_xref="taxon:9606" /tissue\_type="embryonic stem cells, .642 Score 214; DB; Pred. No. 6.6 0; Mismatches 642 bp 42 bp. mRNA linear EST 16 sapiens cDNA 5', mRNA sequence. 6.6e-51; DB 7; Length 642; Mandalam, R., cell lines H1, EST 16-MAY-2004 ۰, Fisk, G. Gaps Н7, 60

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- Web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2380)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 division of Invitrogen
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished
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/mol_type="mRNA"
/db_xref="texon:9606"
/clone="CSODF033YK03"
/tissue_type="Fetal brain"
/plasmid="pCMVSPORT_6"
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Homo sapiens (human)
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lst strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invirogen.
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Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished
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full-length cDNA clone
(human).
                 Homo sapiens
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2 (bases 1 to 2383)
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Eukaryota; Metazoa; Chordata;
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/tissue_type="Neuroblastoma
/plasmid="pCMVSPORT_6"
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CR608110.1 GI:50488917
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1 (bases 1 to 2391)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five end enriched, double-strand cDNA was digested with Not I and cinto the Not I and EcoR V sites of the pCMVSPORT 6 vector. Lik was normalized. Library was constructed by Life Technologies, division of Invitrogen.
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                                                                          Contact : Feng Liang Email : fliang@lifetech.com http://fulllength.invitrogen.com/ InVitroGen Corp
                                                                                                                                                                                               Homo sapiens (human)
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/tissue_type="Fetal brain"
/plasmid="pCMVSPORT_6"
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/mol_type="mRNA"
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Best Local Similarity
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invirogen.
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Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2396)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prend enriched, double-strand cDNA was digested with Not I and clointo the Not I and EcoR V sites of the pCMVSPORT 6 vector. Libra was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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/organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:9606"
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(E-mail : seqref@genoscope.cns.f)
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five end enriched, double-strand cDNA was digested with Not I and into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Li was normalized. Library was constructed by Life Technologies,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 2398)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
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CR618761
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact : Feng Liang Email : fliang@lifetech.com URL : http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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                                                                                                                                          /organism="Homo sapiens"
/mol type="mRNA"
/db_Xref="taxon:9606"
/clone="CSODN003YF07"
/tissue_type="Adult brain"
/plasmid="pCMVSPORT_6"
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/clone="CS0DF007YE19"
/tissue_type="Fetal brain"
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- Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Contact : Peng Liang Email : fliang@lifetech.com URL
Contact : Peng Liang Email : fliang@lifetech.com URL
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1 (bases 1 to 2398)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Princh Liength CDNA libraries and normalization
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/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Homo sapiens (human)
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BP 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.
BP 191006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prend enriched, double-strand cDNA was digested with Not I and clowed enriched, double-strand cDNA was digested with Not I and clowed into the Not I and ECOR V sites of the pCMVSPORT 6 vector. Librates normalized. Libraty was constructed by Life Technologies, a
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full-length
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http://fulllength.invitrogen.com/ InVitroGen Corporation 1600
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF021Y109"
/tissue_type="Fetal brain"
/plasmid="pCMVSPORT_6"
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(E-mail : segref@genoscope.cns.fi
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Mammalia; Eutheria; Primates; Catarrhini; Hor

1 (bases 1 to 2401)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization
                                                                                                       Bukaryota; Metazoa; Chordata; Craniata; Vert. Mammalia; Eutheria; Primates; Catarrhini; Hoi Loses I to 2409)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization
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1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pcMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a
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Location/Qualifiers
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   Genoscope
                                                    Contact : Feng Liang Email : flian http://fulllength.invitrogen.com/
                                                                                      Unpublished
                                                                                                                                                                                                                                      CR624878.1 GI:50505685
HTC; CNSLT_cDNA.
                                                                                                                                                                                                                                                                                                          CR624878 2409 bp 1
full-length cDNA clone CS0DF012YA23
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                                   Faraday Avenue
                                                                                                                                                                                                    Homo sapiens
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Conservative 0;
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/tissue_type="Placenta"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 7.9e-51;
0; Mismatches 0;
                                                        fliang@lifetech.
.com/ InVitroGen
                                                                                                                                                                Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
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3 of Fetal brain
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60 0;

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                             Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
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HTC; CNSLT_cDNA.
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full-length cDNA clone
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                Direct Submission
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/mol type="mRNA"
/db_xref="taxon:9606"
/clone="CSODF012XA23"
/tissue_type="Fetal_brain"
/plasmid="pCMVSPORT_6"
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                Location/Qualifiers
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                                                                                                                                                                                                                                                                                            Feng Liang Email : fliang@lifetech.com URL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GI:50484619
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Pred. No. 7.9e-51;
D; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
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1 (Dases 1 to 356)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R.
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CB112917
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence stop: 356.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kim, Y.S.
21C Frontier Korean EST
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Email: yongsung@mail.kribb.re.kr
Plate: 10 row: A column: 11
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ilarity 100.0%;
Conservative (
/Gell lines"Cho-CK"

//lab host="ToplOF",

//lab host="ToplOF",

//lab host="ToplOF",

//clone lib="EcChocKO"

//note="Organ: Liver; Vector: pCNS-D2; Site_1: EcoRI;

//note="Or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="mRNA"
/db_Xref="taxon:9606"
/clone="CSODF020VJ02"
/tissue_type="Fetal_brain"
/plasmid="pCMVSPORT_6"
                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                  sex="M"
                                                                                                                                                                                                                                                                                                                                                                                                                        clone="L6ChoCK0-10-A11"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Project
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ORIGIN

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VERSION
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Best Local Similarity
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Homo sapiens cDNA clone b
BQ639435
BQ639435.1 GI:21763894
EST.
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1 (bases 1 to 493)

Wistow,G., Bernstein,S.L., Wyatt,M.K., Ray,S., Behal,A.,
Touchman,J.W., Bouffard,G., Smith,D. and Peterson,K.
Expressed sequence tag analysis of human retina for the NEIBank
Project: Retbindin, an abundant, novel retinal cDNA and alternative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 ATAACGGCTAGCCTGAGGAGCTGCTGCGACAGTCCACTATTTTTCGAGAGTGACTCCC
                                                                                                                                                                                                                                                                                                                                                                                    Section on Molecular Structure and Function National Eye Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           splicing of other retina-preferred gene transcripts
Mol. Vis. 8 (4), 196-204 (2002)
22103461
                                                                                                                                                                                                                                                                                  Email: graeme@helix.nih.gov
Plate: 15 row: e column:
                                                                                                                                                                                                                                                                                                                        Tel: 301 402 3452
Fax: 301 496 0078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                   Contact: Wistow G
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                                                                                                                                                                                                                                                       primer: M13RP1 reverse primer (ABI).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of EcoRI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method: The obtained cDNA vectors were used for transformation of competent cells E. coli ToplOF' by electroporation method. The cDNA libraries constructed by this method are full-length enriched cDNA library."
/clone lib="Human Retina cDNA (Un-normalized,
unamplīfied): hd/he"
/note="Organ: Eye; Vector: pSPORT1; Neural re
                                                              /tissue_type="Retina"
/dev_stage="Adult"
/lab_host="EMDH10B"
                                                                                                                            /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="he15e11"
                                                                                                                                                                                                                                   ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                  Bethesda, MD
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Pred. No. 1.7e-50;
0; Mismatches 1
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a cDNA (Un
e he15ell
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(Un-normalized, unamplified): hd/he
ell 5', mRNA sequence.
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SOURCE

Pocus

COMMENT

Eye; Vector: pSPORT1; Neural retina tissue

TITLE

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REFERENCE
AUTHORS
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VERSION
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CB154948
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JOURNAL
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Best Local Similarity
Matches 213; Conser
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                                                                                                                                                                                                                                                                                                Genome Research Center
Korea Research Institute of Bioscience & Biotechnology
52 Eoeun-dong Yuseong-gu, Daejeon 305-333, South Korea
Tel: +82-42-860-4470
Fax: +82-42-860-4409
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 511)

Kim,N.S., Hahn,Y., Oh,J.H., Lee,J.Y., Ahn,H.Y., Chu,M.Y., Kim,M.R. Oh,K.J., Cheong,J.E., Sohn,H.Y., Kim,J.M., Park,H.S., Kim,S. and Ch,K.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                             21C Frontier Korean EST
Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CB154948
CB154948.1
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K-EST0213039 B2N807043 Homo sapiens
                                                                                                                                                                                                                                                         Email: yongsung@mail.kribb.re.kr
Plate: 30 row: G column: 11
                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Kim YS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA sequence.
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                                                                                                                                                                                                         e: 30 row: G column: 11 quality sequence stop: 511. Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      primer-adapter
[5'-pGACTAGTTCTAGATCGCGAGCGGCCCCC(T)15-3']. EST analysis
was performed on the unamplified library at the NIH
Intramural Sequencing Center (NISC)."
                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/lab_host="Top10F/"
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/note="Organ: Brain; Vector: pCNS-D2; Site_1: EcoRI;
                                                                   'sex="M"
                                                                                            'clone="B2N807043-30-G11"
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Pred. No. 1.8e-50;
0; Mismatches 1
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Site\_2: NotI; The poly (A)+ RNA was dephosphorylated with bacterial alkaline phosphatase (BAP) and then decapped with tabacco acid pyrophosphatase (TAP). The decapped intact mRNA was ligated with DNA-RNA linker including ECORI site by treatment of T4 RNA linker including ECORI site by treatment of T4 RNA ligase and the first strand cDNA was synthesized from oligo dT-selected mRNA by priming with dT-tailed vector. The dT-tailed vector was adjusted to have about 60nt. The cDNA vector was circularized with E. coli DNA ligase after digestion of ECORI which site is also included in vector. An RNA strand converted to a DNA strand by Okayama-Berg method. The obtained cDNA vectors were used for transformation of competent cells E. coli Toploff by electroporation method. The cDNA libraries constructed by this method are

유정 B 5 밁 Ś 밁 Query Match 98.8%; Score 212.4; DB 6; Length 511; Best Local Similarity 99.5%; Pred. No. 1.8e-50; Matches 213; Conservative 0; Mismatches 1; Indels 0 181 TCTCAGAGCCGAGCCGACAGAGAGCAGGGAACCG 214 181 121 121 61 61 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTCCGGTTTCCAGCCCCCAA 180 GTTGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT GITGTCCCAAGGCTTCCCAGAGCGAACCTGTGCGGCTGCAGGCACCGGCGCGTCGAGTTT TCTCAGAGCGGAGCCGACAGAGAGCAGCGAACCG 214 CCGGCGTCCGGAAGGACCGAGCTCTTCTCGCGGATCCAGTGTTTCCGGTTTTCCAGCCCCCAA 180 0, Gaps 120 120 60 60 0

Search completed: February 11, 2005, 09:02:43 Job time : 1646 secs